



V F H S V G N L E T L I L D S N P L A C	367
GTC TTC CAC TCG GTG GGC AAC CTG GAG ACA CTC ATC CTG GAC TCC AAC CCG CTG GCC TGC	1231
D C R L L W V F R R R W R L N F N R Q Q	387
GAC TGT CCG CTC CTG TGG GTG TTC CCG CGC CGC TGG CCG CTC AAC TTC AAC CCG CAG CAG	1291
P T C A T P E F V Q G K E F K D F P D V	407
CCC ACG TCG GCC ACG CCC GAG TTT GTC CAG GGC AAG GAG TTC AAG GAC TTC CCT GAT GTG	1351
L L P N Y F T C R R A R I R D R K A Q Q	427
CTA CTG CCC AAC TAC TTC ACC TGC CGC CGC GCC CGC ATC CCG GAC CGC AAG GCC CAG CAG	1411
V F V D E G H T V Q F V C R A D G D P P	447
GTG TTT GTG GAC GAG GGC CAC ACG GTG CAG TTT GTG TGC CCG GCC GAT GGC GAC CCG CCG	1471
P A I L W L S P R K H L V S A K S N G R	467
CCC GCC ATC CTC TGG CTC TCA CCC CGA AAG CAC CTG GTC TCA GCC AAG AGC AAT GGG CCG	1531
L T V F P D G T L E V R Y A Q V Q D N G	487
CTC ACA GTC TTC CCT GAT GGC ACG CTG GAG GTG CGC TAC GCC CAG GTA CAG GAC AAC GGC	1591
T Y L C I A A N A G G N D S M P A H L H	507
ACG TAC CTG TGC ATC CCG GCC AAC GCG GGC GGC AAC GAC TCC ATG CCC GCC CAC CTG CAT	1651
V R S Y S P D W P H Q P N K T F A F I S	527
GTG CCG AGC TAC TCG CCC GAC TGG CCC CAT CAG CCC AAC AAG ACC TTC GCT TTC ATC TCC	1711
N Q P G E G E A N S T R A T V P F P F D	547
AAC CAG CCG GGC GAG GGA GAG GCC AAC AGC ACC CGC GCC ACT GTG CCT TTC CCC TTC GAC	1771
I K T L I I A T T M G F I S F L G V V L	567
ATC AAG ACC CTC ATC ATC GCC ACC ACC ATG GGC TTC ATC TCT TTC CTG GGC GTC GTC CTC	1831
F C L V L L F L W S R G K G N T K H N I	587
TTC TGC CTG GTG CTG CTG TTT CTC TGG AGC CGG GGC AAG GGC AAC ACA AAG CAC AAC ATC	1891
E I E Y V P R K S D A G I S S A D A P R	607
GAG ATC GAG TAT GTG CCC CGA AAG TCG GAC GCA GGC ATC AGC TCC GCC GAC GCG CCC CGC	1951
K F N M K M I *	615
AAG TTC AAC ATG AAG ATG ATA TGA	1975
GGCCGGGGGGGGGGCAGGACCCCCGGGGGGGGGGCAGGGGAAGGGGGCTGGCCGGCCACCTGCTCACTCTCCAGTCC	2054
TTCCCACTCTCTCCCTAGCCCTTCTACACAGTTCCTCTTTCTCCCTCCCGCTCCGTCCCTGCTGCCCCCGCCAGCC	2133
CTCACCACCTGCCCTCTCTTCTACAGGACCTCAGAAGCCCAGACCTGGGGACCCACCTACACAGGGGCATTGACAGAC	2212
TGGAGTTTAAAGCCGACGACCGGACCGGGCAGAGTCAATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACTTG	2291
GGTTTCAATAATTATGGATTTTTATGAAAACCTGAAATAATAAAAAAAAAAAAAAAAAAAG	2351

[illegible][illegible]

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Fig 3

Percent Similarity:

ty: 29.412

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T79      1 MLAG .....LACWQPILLVLGSLVSGS..ATGCPPRCECSAQDR. 47
          : . . . . . || | : | | : . : | . . : | | . | | . . :
D45913    1 .....MARLSTGKAAC.QVVLGLLITSLTESSILTSECPQLCVCEIRPWF 44

T79      48 .....AVLCHRKRFFVAVPEGIPTETRLLDLGKNRIKTLNQDEFAS 87
          . | | : | : . : | : . . : | : | | . | | . |
D45913    45 TPQSTYREATTVDCLRLTRIPGNLSSDTQVLLQLQSNNI..... 84

T79      88 FPHLEELNENIVSAVEPGAFFNNLFLNRLTLGLRSNRLKLIPLGVFTGLS 137
          | . . . . . | | | | . | : . . | : . . | . . . . . |
D45913    85 .....AKTVDELQQLFNLTDELDFSQNNFTNIKEVGLANLT 119

T79      138 NLTKLDTRENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRAFSGLNLSL 187
          . | | . | | . | : | | : | | | | . | : . : | | . | | | | . |
D45913    120 QLTTLHLEENQISEMTDYCLQDLSNLQELYINHQNQISTISANAFSGLKNL 169

T79      188 EQLTLEKCNLTISIPTALSHLHGLIVLRLRHLNINAIIRDYSFKRLYRLKV 237
          . | | : . | . | . . . . | : | : . . : : | | . | : | . | :
D45913    170 LRLHLNSNKLKVIDSRWFDSTPNLEILMIGENFVIGILDMNFRPLSNLRS 219

T79      238 LEISHWPYLDTMTFNCLYGLN.LTSLSITHCNLTAVPYLAVRHLVYLRFL 286
          | : . | | . . . . | | | : | | | : . . | . | | | : . . | : |
D45913    220 LVLG.MYLTQVPGNALVGLDSLESLSFYDNKLIKVPQLALQKVPNLKFL 268

T79      287 NLSYNPISTIEGSMHELLRLQEIQLVG.GQLAVVEPY..... 323
          : | . | | | . | : : : : : | | | : : . | : | . | : |
D45913    269 DLNKNPIHKIQEGDFKNMLRLKELGINNMGELVSVDRYALDNLPELTKE 318

T79      324 .....AFRGLNYLRVLNVSGNQLTLEESVFSVGNLETIL 360
          | | | : : | | : . | . | : : . . . . | : | | : : :
D45913    319 ATNNPKLSYIHLAFRSVPALSLMLNNNALNAVYQKTVESLPNLREISI 368

T79      361 DSNPLACDCRLLWVFRWRRLNFRNRQPT.CATPEFVQGKEFKDFPDVLL 409
          . | | | | | | : | : . . : . | . . | | | . | : . | : | :
D45913    369 HSNPLRCDCVIHWINSNKTNIIRFMEPLSMFCAMPPEYRGQOVK...EVLI 415

T79      410 PNYFT.CRRARIRDRKAQVVFVDEGHTVQFVCRADGDPFPAILWLSPRKH 458
          . : . | . . : | : : : : | | | : : | | | : : | . | . | : : |
D45913    416 QDSSEQCLPMISHDTFPNHLNMDIGTTLFLDCRAMAEPEPEIYWVTPIGN 465

T79      459 LVSAKS.NGRLTVFPDGTLEVRYAQVQDNGTYLCIAANAGGND SMPAHLH 507
          : . . . . . : : : : : | | | : | : | . | | : | . | . | . | : .
D45913    466 KITVETLSDKYKLSSEGTL EIANIQIEDSGRYTCVAQNVQGADTRVATIK 515

T79      508 V.....RSYSPDWPHQ 518
          | : . . . . .
D45913    516 VNGTLLDGAQVLKIYVKQTESHSILVSWKVNSNVMTSNLKWSSATMKIDN 565

T79      519 PNKTF.....AFISNQPGEGEANSTRA 540

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FIG. 3 (1 of 2)

D45913 566 PHITYTARVPVDVHEYNLHLQ PSTDYEVCLTVSNIHQQTQKSCVNVTTK 615  
 T79 541 TVPFPFDIKTLIIATTMGFI..SFLGVVLFCLVLLFLWSRGKGNTKHNIE 588  
 D45913 616 TAAFALDISDHETSTALAAVMGSMFAVISLASIAIYIAKRFRKKNYHHSL 665  
 T79 589 IEYVPRKSDAGISSADAPRKFNMKMI..... 614  
 D45913 666 KKYMQKTSSIPLNEL.YPPLINLWEADSDKDKDGSADTKPTQVDTSRSYY 714

FIG. 3 (2 of 2)

451  
751  
4.44

100-443887-100



P D S T S V C V Q G Q C V K A G C D R I	399
CCA GAT TCC ACC TCT GTC TGT GTG CAA GGA CAG TGT GTA AAA GCT GGT TGT GAT CGC ATC	1199
I D S K K K F D K C G V C G G N G S T C	419
ATA GAC TCC AAA AAG AAG TTT GAT AAA TGT GGT GTT TGC GGG GGA AAT GGA TCT ACT TGT	1259
K K I S G S V T S A K P G Y H D I I T I	439
AAA AAA ATA TCA GGA TCA GTT ACT AGT GCA AAA CCT GGA TAT CAT GAT ATC ATC ACA ATT	1319
P T G A T N I E V K Q R N Q R G S R N N	459
CCA ACT GGA GCC ACC AAC ATC GAA GTG AAA CAG CGG AAC CAG AGG GGA TCC AGG AAC AAT	1379
G S F L A I K A A D G T Y I L N G D Y T	479
GGC AGC TTT CTT GCC ATC AAA GCT GCT GAT GGC ACA TAT ATT CTT AAT GGT GAC TAC ACT	1439
L S T L E Q D I M Y K G V V L R Y S G S	499
TTG TCC ACC TTA GAG CAA GAC ATT ATG TAC AAA GGT GTT GTC TTG AGG TAC AGC GGC TCC	1499
S A A L E R I R S F S P L K E P L T I Q	519
TCT GCG GCA TTG GAA AGA ATT CGC AGC TTT AGC CCT CTC AAA GAG CCC TTG ACC ATC CAG	1559
V L T V G N A L R P K I K Y T Y F V K K	539
GTT CTT ACT GTG GGC AAT GCC CTT CGA CCT AAA ATT AAA TAC ACC TAC TTC GTA AAG AAG	1619
K K E S F N A I P T F S A W V I E E W G	559
AAG AAG GAA TCT TTC AAT GCT ATC CCC ACT TTT TCA GCA TGG GTC ATT GAA GAG TGG GGC	1679
E C S K T C G K G Y K K R S L K C L S H	579
GAA TGT TCT AAG ACC TGT GGG AAG GGT TAC AAA AAA AGA AGC TTG AAG TGT CTG TCC CAT	1739
D G G V L S H E S C D P L K K P K H F I	599
GAT GGA GGG GTG TTA TCT CAT GAG AGC TGT GAT CCT TTA AAG AAA CCT AAA CAT TTC ATA	1799
D F C T M A E C S *	609
GAC TTT TGC ACA ATG GCA GAA TGC AGT TAA	1829
GTGGTTAAGTGGTGTAGCTCTGAGGGCAAGGCCAAAGTGAGGAAGGGCTGGTGCAGGGAAAGCAAGAAGCGCTGGAGGG	1908
ATCCAGCGTATCTTGCCAGTAACCACTGAGGTGTATCAGTAAGGTGGATTATTGGGGGTAGATAGAAAAGGAGTTGAAT	1987
CATCAGAGTAAACTGCCAGTTGCCAAATTTGATAGGATAGTTAGTGAGGATTATTAACTCTGAGCAGTGATATAGCATA	2066
ATAAAGCCCCGGGCATTATTATTATTATTCTTTTGTGTACATCTATTACAAGTTTAGAAAAACAAAGCAATTGTCAAA	2145
AAAAGTTAGAAGTATTACAACCCCTGTTTCCTGTTACTTATCAAATACTTAGTATCATGGGGGTGGGAAATGAAAAGT	2224
AGGAGAAAAGTGAGATTTTACTAAGACCTGTTTACTTTACCTCACTAACAATGGGGGGAGAAAGGAGTACAATAGGA	2303
TCFTTGACCAGCACTGTTTATGGCTGCTATGGTTTCAGAGAATGTTTATACATTATTTCTACCGAGAATTAAAAGTTCA	2382
GATTGTTCAACATGAGAGAAAAGGCTCAGCAACGTGAAATAACGCAATGGCTTCTCTCTTTTGGACCATCTCA	2461
GTCTTTATTGTGTAAATTCATTTTGAGGAAAAACAACCTCCATGTATTTATTCAAGTGCATTAAAGTCTACAATGGAAA	2540
AAAAGCAGTGAAGCATTAGATGCTGGTAAAAGCTAGAGGAGACACAATGAGCTTAGTACCTCCAACCTCTCTTTCTCTTC	2619
TACCATGTAACCCCTGCTTTGGGAATATGGATGTAAAGAAGTAAGTGTGTCTCATGAAAATCAGTACAATCACACAAGG	2698



AGGATGAAACGCCCGACAAAAATGAGGTGTGTAGAACAGGGTCCCA.CAGGTTTGGGGACATTGAGATCACTTGTCTTG	2777
TGGTGGGGAGGCTGCTGAGGGGTAGCAGGTCCATCTCCAGCAGCTGGTCCAACAGTCGTATCCGGTGAATGTCGTCTC	2856
AGCTCTTCTGTGAGAATATGATTTTTTCCATATGTATATAGTAAATATGTTACTATAAAATTACATGTACTTTATAAGT	2935
ATTGGTTTGGGIGTTCCCTCCAGAAGGACTATAGTTAGTAATAAATGCCTATAATAACATATTTATTTTTTATACATTT	3014
ATTTCTAATGAAAAAACTTTTAAATTATATCGGTTTTGTGGAAGTGCATATAAAATAGAGTATTTATACAATATATGT	3093
TACTAGAAATAAAAGAACACTTTTTGGAAAAAAGGGCGGCGCGC	3147

**FIG. 5 (3 of 3)**

TANGO 71/ADAMTS-1 Comparison (90% Protein Sequence Identity)

```

251 DQSMADFHGSGGLKHYLLTLFSVAARFYKHPSTIRNSISLVVVKILVTYEEQ 300
      ||||:|
1 .....TRPILVTHDEQ 11

301 KGPEVTSNAALTLRNFCNMQKQHNPSDRDPEHYDTAILFTQDLCGSHT 350
      |||||:|
12 KGPEVTSNAALTLRNFCNMQKQHNPPSDRDAEHYDTAILFTQDLCGSQT 61

351 CDTLGMADVGTVCDFSRSCSVTEDDGLQAFTTAHELGHVFNMPHDDAKH 400
      |||||:|
62 CDTLGMADVGTVCDFSRSCSVTEDDGLQAFTTAHELGHVFNMPHDDAKQ 111

401 CASLNGVSGDSHMASMLSSLDHSQFWSFCSAYMVTSLDNGHGECLEMDK 450
      |||||:|
112 CASLNGVNDQSHMASMLSNLDHSQFWSFCSAYMITSLDNGHGECLEMDK 161

451 PQNPILKPSDLPGTLYDANRQCQFTFGESKHCPEAASTCTLWCTGTSG 500
      |||||:|
162 PQNPILKPSDLPGTLYDANRQCQFTFGESKHCPEAASTCTLWCTGTSG 211

501 GLLVCQTKHFPWADGTSCEGEGKWCVSGKCVNKTMDKHFPVHGSWGWG 550
      |||||:|
212 GLLVCQTKHFPWADGTSCEGEGKWCVSGKCVNKTMDKHFPVHGSWGMG 261

551 PWGDCSRTCGGGVQYTMRECNFVFKNGGKYCEGKRVRYRSCNIEDCPDN 600
      |||||:|
262 PWGDCSRTCGGGVQYTMRECNFVFKNGGKYCEGKRVRYRSCNIEDCPDN 311

601 NGKTFREEQCEAHNEFSKASFGNEPTVEWTFKYAGVSPKDRCKLTCEAKG 650
      |||||:|
312 NGKTFREEQCEAHNEFSKASFGSGPAVEWTFKYAGVSPKDRCKLTCEAKG 361

651 IGYFFVLQPKVVDGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKFDKCGV 700
      |||||:|
362 IGYFFVLQPKVVDGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKFDKCGV 411

701 CCGNGSTCKKMSGIVTSTRPGYHDIITIPAGATNIEVKHNRQGSRNNGS 750
      |||||:|
412 CCGNGSTCKKLSGVS TSAKPGYHDIITIPAGATNIEVKHNRQGSRNNGS 461

751 FLAIRAADGTYTLNGFTLSTLEQDLTYKGVVLRYSGSSAALERIRSFSP 800
      |||||:|
462 FLAIRAADGTYTLNGFTLSTLEQDLTYKGVVLRYSGSSAALERIRSFSP 511

801 LKEPLTIQVLMVGHALRPKIKTYFMKKKTESFNAIPTFSEWVIEWEGEC 850
      |||||:|
512 LKEPLTIQVLMVGHALRPKIKTYFMKKKTESFNAIPTFSEWVIEWEGEC 560

901 WSPCKSTCGKGYKKRSLKCVSHDGGVLSNESCDPLKKPKHYIDFCTLTQC 950
      |||||:|
561 ...CKSTCGKGYKKRSLKCVSHDGGVLSNESCDPLKKPKHYIDFCTMAEC 607

951 S* 951
      |
608 S* 609

```

FIG. 6

gtgcctac atg gtc acg tcc ttc cta gat aat gga cac ggg gaa tgt ttg	50
Met Val Thr Ser Phe Leu Asp Asn Gly His Gly Glu Cys Leu	
1 5 10	
atg gac aag ccc cag aat cca atc aag ctc cct tct gat ctt ccc ggt	98
Met Asp Lys Pro Gln Asn Pro Ile Lys Leu Pro Ser Asp Leu Pro Gly	
15 20 25 30	
acc ttg tac gat gcc aac cgc cag tgt cag ttt aca ttc gga gag gaa	146
Thr Leu Tyr Asp Ala Asn Arg Gln Cys Gln Phe Thr Phe Gly Glu Glu	
35 40 45	
tcc aag cac tgc cct gat gca gcc agc aca tgt act acc ctg tgg tgc	194
Ser Lys His Cys Pro Asp Ala Ala Ser Thr Cys Thr Thr Leu Trp Cys	
50 55 60	
act ggc acc tcc ggt ggc tta ctg gtg tgc caa aca aaa cac ttc cct	242
Thr Gly Thr Ser Gly Gly Leu Leu Val Cys Gln Thr Lys His Phe Pro	
65 70 75	
tgg gca gat ggc acc agc tgt gga gaa ggg aag tgg tgt gtc agt ggc	290
Trp Ala Asp Gly Thr Ser Cys Gly Glu Gly Lys Trp Cys Val Ser Gly	
80 85 90	
aag tgc gtg aac aag aca gac atg aag cat ttt gct act cct gtt cat	338
Lys Cys Val Asn Lys Thr Asp Met Lys His Phe Ala Thr Pro Val His	
95 100 105 110	
gga agc tgg gga cca tgg gga ccg tgg gga gac tgc tca aga acc tgt	386
Gly Ser Trp Gly Pro Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys	
115 120 125	
ggt ggt gga gtt caa tac aca atg aga gaa tgt gac aac cca gtc cca	434
Gly Gly Gly Val Gln Tyr Thr Met Arg Glu Cys Asp Asn Pro Val Pro	
130 135 140	
aag aac gga ggg aag tac tgt gaa ggc aaa cga gtc cgc tac agg tcc	482
Lys Asn Gly Gly Lys Tyr Cys Glu Gly Lys Arg Val Arg Tyr Arg Ser	
145 150 155	
tgt aac atc gag gac tgt cca gac aat aac gga aaa acg ttc aga gag	530
Cys Asn Ile Glu Asp Cys Pro Asp Asn Asn Gly Lys Thr Phe Arg Glu	
160 165 170	
gag cag tgc gag gcg cac aat gag ttt tcc aaa gct tcc ttt ggg aat	578
Glu Gln Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Asn	
175 180 185 190	
gag ccc act gta gag tgg aca ccc aag tac gcc ggc gtc tcg cca aag	626
Glu Pro Thr Val Glu Trp Thr Pro Lys Tyr Ala Gly Val Ser Pro Lys	
195 200 205	

Fig. 7 (1 of 4)

gac agg tgc aag ctc acc tgt gaa gcc aaa ggc att ggc tac ttt ttc	674
Asp Arg Cys Lys Leu Thr Cys Glu Ala Lys Gly Ile Gly Tyr Phe Phe	
210 215 220	
gtc tta cag ccc aag gtt gta gat ggc act ccc tgt agt cca gac tct	722
Val Leu Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser	
225 230 235	
acc tct gtc tgt gtg caa ggg cag tgt gtg aaa gct ggc tgt gat cgc	770
Thr Ser Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg	
240 245 250	
atc ata gac tcc aaa aag aag ttt gat aag tgt ggc gtt tgt gga gga	818
Ile Ile Asp Ser Lys Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly	
255 260 265 270	
aac ggt tcc aca tgc aag aag atg tca gga ata gtc act agt aca aga	866
Asn Gly Ser Thr Cys Lys Lys Met Ser Gly Ile Val Thr Ser Thr Arg	
275 280 285	
ccc ggg tat cat gac att gtc aca att cct gct gga gcc acc aac att	914
Pro Gly Tyr His Asp Ile Val Thr Ile Pro Ala Gly Ala Thr Asn Ile	
290 295 300	
gaa gtg aaa cat cgg aat caa agg ggg tcc aga aac aat ggc agc ttt	962
Gln Val Lys His Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe	
305 310 315	
ctg gct att aga gcc gct gat ggt acc tat att ctg aat gga aac ttc	1010
Leu Ala Ile Arg Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asn Phe	
320 325 330	
act ctg tcc aca cta gag caa gac ctc acc tac aaa ggt act gtc tta	1058
Thr Leu Ser Thr Leu Glu Gln Asp Leu Thr Tyr Lys Gly Thr Val Leu	
335 340 345 350	
agg tac agt ggt tcc tcg gct gcg ctg gaa aga atc cgc agc ttt agt	1106
Arg Tyr Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser	
355 360 365	
cca ctc aaa gaa ccc tta acc atc cag gtt ctt atg gta ggc cat gct	1154
Pro Leu Lys Glu Pro Leu Thr Ile Gln Val Leu Met Val Gly His Ala	
370 375 380	
ctc cga ccc aaa att aaa ttc acc tac ttt atg aag aag aag aca gag	1202
Leu Arg Pro Lys Ile Lys Phe Thr Tyr Phe Met Lys Lys Lys Thr Glu	
385 390 395	
tca ttc aac gcc att ccc aca ttt tct gag tgg gtg att gaa gag tgg	1250
Ser Phe Asn Ala Ile Pro Thr Phe Ser Glu Trp Val Ile Glu Glu Trp	
400 405 410	

Fig. 7 (2 of 4)

ggg gag tgc tcc aag aca tgc ggc tca ggt tgg cag aga aga gta gtg 1298  
 Gly Glu Cys Ser Lys Thr Cys Gly Ser Gly Trp Gln Arg Arg Val Val  
 415 420 425 430

cag tgc aga gac att aac gga cac cct gct tcc gaa tgt gca aag gaa 1346  
 Gln Cys Arg Asp Ile Asn Gly His Pro Ala Ser Glu Cys Ala Lys Glu  
 435 440 445

gtg aag cca gcc agt acc aga cct tgt gca gac ctt cct tgc cca cac 1394  
 Val Lys Pro Ala Ser Thr Arg Pro Cys Ala Asp Leu Pro Cys Pro His  
 450 455 460

tgg cag gtg ggg gat tgg tca cca tgt tcc aaa act tgc ggg aag ggt 1442  
 Trp Gln Val Gly Asp Trp Ser Pro Cys Ser Lys Thr Cys Gly Lys Gly  
 465 470 475

tac aag aag aga acc ttg aaa tgt gtg tcc cac gat ggg ggc gtg tta 1490  
 Tyr Lys Lys Arg Thr Leu Lys Cys Val Ser His Asp Gly Gly Val Leu  
 480 485 490

tca aat gag agc tgt gat cct ttg aag aag cca aag cat tac att gac 1538  
 Ser Asn Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Tyr Ile Asp  
 495 500 505 510

ttc tgc aca ctg aca cag tgc agt taagaggcgt tagaggacaa ggtagcgtgg 1592  
 Phe Cys Thr Leu Thr Gln Cys Ser  
 515

gga ggggctg atacactgag tgcaagagta ctggagggat ccagtgagtc aaaccagtaa 1652  
 gca gtagggt gtggcaagga ggtgtgtgta ggggatacat agcaaaggag gtagatcagg 1712  
 aca ctacct gccagttaca ttctgataag gtagttaatg aggcacagta gcatctgaaa 1772  
 gag catacag agcactaagg agccccaagg cactattagt atctcttttc ttatatctat 1832  
 cgc ccaata attttcagag tctggcagaa gccctgttgc actgtactaa ctagatactt 1892  
 ctt atcacaa agattgggaa aggcaaagca gaaagatggg aagactgggt ttcaaacaag 1952  
 gct tgggtttc aatcactgga ggcaaggagg aggggacaaa caagatcatt attcgaagtc 2012  
 gct ggttgct gtggttttac ggaagggtga tgcattcatt ctatcaacag tgaaaagttc 2072  
 agctt gttca acgtgacaga aaggctcatc tccgtgaaag agctcctgat ttcttcttac 2132  
 accatctcag ttcttaacta tagttcatgt tgaggtagaa acaattcatc tatttataaa 2192  
 atgtacattg gaaaaaaaaa gtgaagttta tgaggtagac ataaaaactg aaggaaacaa 2252  
 tgagcaacat gcctcctgct ttgcttcctc ctgaggtaaa cctgcctggg gattgagggt 2312  
 gtttaagatt atccatggct cacaagaggc agtaaaaataa tacatgttgt gccagagtta 2372  
 gaatggggta tagagatcag ggtcccatga gatggggaac atggtgatca ctcatctcac 2432  
 atgggagggt gctgcagggt agcagggtcca ctctggcag ctggtccaac agtcgtatcc 2492  
 tggatgaatgt ctgttcagct cttctactga gagagaatat gactgtttcc atatgtatat 2552  
 gtatatagta aaatatgtta ctatgaattg catgtacttt ataagtattg gtgtgtctgt 2612  
 tccttctaag aaggactata gtttataata aatgcctata ataacatatt tatttttata 2672  
 catttatttc taatgataaa acctttaagt tatatcgctt ttgtaaaagt gcatataaaa 2732  
 atagagtatt tacaataat atgttaacta gaaataataa aagaacactt ttgaatgtgt 2792  
 atgcctattt tctggagtgg gattaacttc tgggcaagaa atctgatgag acacaaacat 2852  
 tggacttcaa gacagtttta aattttgggt aaatgaactg tatttcctgt ttatagacgt 2912  
 actaataaaa aagaagttga tgatgtcttt agtggttaaga ttgttactaa tgtggttggc 2972  
 aaattgctgt aaagagccag atagtaagca tttatggcat tgtaggctat ctttcctgcc 3032  
 acaaccatgt gacagtgagt gctttgtagg actgagagca gccataaatg acatgtaaat 3092

Fig. 7 (3 of 4)

gataaactgt ggctgtgctt taataaaaact ttatttaca aaaaaaaaaa aaa

3145

gataaactgt ggctgtgctt taataaaaact ttatttaca aaaaaaaaaa aaa

```

gcgggccgctc cgggcccggcc caagggacag agccagggctc cgggagcccg caacactcgt 60
cctgagagacc cgggctcctc agcccgctac ggccaggggcc tgggctccg cccccgactc 120
ccgagctcctt gccctagagt cgactggggt cccggccgcg tgggacagac agacggacag 180
ccagccctgc gagggcgcgcg ggaccgggcg gaggtgtgtg aggaggagac cgaggagggg 240
ggctgggctg gggctggggc cgcgccggca agagagacat gcgattgggtg accaagccga 300
gcggacggac agcgcgccc ag atg cag gtg agc gag agg atg ctg gca ggg 352
                Met Gln Val Ser Glu Arg Met Leu Ala Gly
                  1             5             10

ggg atg aga agc atg ccc agc ccc ctc ctg gcc tgc tgg cag ccc atc 400
Gly Met Arg Ser Met Pro Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile
                15             20             25

ctc ctg ctg gta ctg ggc tca gtg ctg tca ggc tct gct aca ggc tgc 448
Leu Leu Leu Val Leu Gly Ser Val Leu Ser Gly Ser Ala Thr Gly Cys
                30             35             40

ccg ccc cgc tgc gag tgc tca gcg cag gac cga gcc gtg ctc tgc cac 496
Pro Pro Arg Cys Glu Cys Ser Ala Gln Asp Arg Ala Val Leu Cys His
                45             50             55

cgc aaa cgc ttt gtg gcg gtg ccc gag ggc atc ccc acc gag act cgc 544
Arg Lys Arg Phe Val Ala Val Pro Glu Gly Ile Pro Thr Glu Thr Arg
                60             65             70

ctg ctg gac ctg ggc aaa aac cgc atc aag aca ctc aac cag gac gag 592
Leu Leu Asp Leu Gly Lys Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu
                75             80             85             90

ttt gcc agc ttc cca cac ctg gag gag cta gaa ctc aat gaa aac atc 640
Phe Ala Ser Phe Pro His Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile
                95             100             105

gtg agc gcc gtg gag cca ggc gcc ttc aac aac ctc ttc aac ctg agg 688
Val Ser Ala Val Glu Pro Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg
                110             115             120

act ctg ggg ctg cgc agc aac cgc ctg aag ctt atc ccg ctg ggc gtc 736
Thr Leu Gly Leu Arg Ser Asn Arg Leu Lys Leu Ile Pro Leu Gly Val
                125             130             135

ttc acc ggc ctc agc aac ttg acc aag ctg gac atc agt gag aac aag 784
Phe Thr Gly Leu Ser Asn Leu Thr Lys Leu Asp Ile Ser Glu Asn Lys
                140             145             150

atc gtc atc ctg cta gac tac atg ttc caa gac cta tac aac ctc aag 832
Ile Val Ile Leu Leu Asp Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys
                155             160             165             170

tcg ctg gag gtc ggc gac aac gac ctc gtc tac atc tcc cat cga gcc 880
Ser Leu Glu Val Gly Asp Asn Asp Leu Val Tyr Ile Ser His Arg Ala
                175             180             185

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**Fig. 8 (1 of 2)**

ttc agc ggc ctc aac agc ctg gaa cag ctg acg ctg gag aaa tgc aat	928
Phe Ser Gly Leu Asn Ser Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn	
190 195 200	
ctg acc tcc atc ccc acg gag gcg ctc tcc cac ctg cac ggc ctc atc	976
Leu Thr Ser Ile Pro Thr Glu Ala Leu Ser His Leu His Gly Leu Ile	
205 210 215	
gtc ctg cgg cta cga cat ctc aac atc aat gcc atc agg gac tac tcc	1024
Val Leu Arg Leu Arg His Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser	
220 225 230	
ttc aag agg ctg tac cga ctt aag gtc tta gag atc tcc cac tgg ccc	1072
Phe Lys Arg Leu Tyr Arg Leu Lys Val Leu Glu Ile Ser His Trp Pro	
235 240 245 250	
tac ctg gac acc ata acc ccc cgg acg cgt ggg tcg ac	1110
Tyr Leu Asp Thr Ile Thr Pro Arg Thr Arg Gly Ser	
255 260	

Fig. 8 (2 of 2)



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ctcctggatg tgcgcagccg cagagcgctg ctgctgtgcc taatacccat cgctgcgcac 60
ttgacagcca gtccgcccgt ccggagcccg gctcgttggg gcagc atg gcg ggg tcg 117
                                     Met Ala Gly Ser
                                     1

ccg ctg ctc tgc ggg ccg cgg gcc ggg ggc gtc ggc att ttg gtg ctg 165
Pro Leu Leu Cys Gly Pro Arg Ala Gly Gly Val Gly Ile Leu Val Leu
   5                10                15                20

ctg ctc ttg ggc ctt ctg agg ctg ccc ccc acc ctg tca gcg agg ccc 213
Leu Leu Leu Gly Leu Leu Arg Leu Pro Pro Thr Leu Ser Ala Arg Pro
      25                30                35

gtg aag gag ccc cgc agt ctg agc gca gca tcc gcg ccc ttg gtt gag 261
Val Lys Glu Pro Arg Ser Leu Ser Ala Ala Ser Ala Pro Leu Val Glu
      40                45                50

acg agc act ccc ctc cgc ttg cgt cgg gcc gtg ccc cga gga gag gcg 309
Thr Ser Thr Pro Leu Arg Leu Arg Arg Ala Val Pro Arg Gly Glu Ala
      55                60                65

gag ggt gcg gtg cag gag ctg gcg cgg gcg ctg gcg cac ctg ctg gag 357
Ala Gly Ala Val Gln Glu Leu Ala Arg Ala Leu Ala His Leu Leu Glu
   70                75                80

gag gag aga cag gaa cgc gcg cgt gct gag gcg cag gag gct gag gat 405
Ala Glu Arg Gln Glu Arg Ala Arg Ala Glu Ala Gln Glu Ala Glu Asp
   85                90                95                100

cag cag gcg cgt gtc ctg gcg cag ctg ctg cgc gcc tgg ggc tct ccg 453
Gln Gln Ala Arg Val Leu Ala Gln Leu Leu Arg Ala Trp Gly Ser Pro
      105                110                115

cgt gcc tcg gac ccg ccc ttg gcc ccc gac gat gac ccg gac gct cca 501
Arg Ala Ser Asp Pro Pro Leu Ala Pro Asp Asp Asp Pro Asp Ala Pro
      120                125                130

gct gca cag ctc gcc cgt gct ctg ctc cga gct cgc cta gac ccc ggc 549
Ala Ala Gln Leu Ala Arg Ala Leu Leu Arg Ala Arg Leu Asp Pro Gly
      135                140                145

ccc cag tgt atg atg atg gcc cca ctg gcc cag acg tcg agg atg ccg 597
Pro Gln Cys Met Met Met Ala Pro Leu Ala Gln Thr Ser Arg Met Pro
      150                155                160

gcg acg aga ctc ctg acg tgg acc ctg agc tgc tgaggtactt gctagggcgg 650
Ala Thr Arg Leu Leu Thr Trp Thr Leu Ser Cys
      165                170                175

atcctcaccg gaagttcgga gccagaggct gctcctgcc cgcgccgcct ccgccgatct 710
gtggaccagg atttgggtcc cgaggtgccc cctgagaacg tactgggggc tctgctacgc 770
gtcaaacgcc tggagaaccc ctgcgccag gcgcgggcac gccgcctcct gcctccctga 830

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**Fig. 9 (1 of 2)**

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gcgatgctgc atcctgcacg ccctggaacc caggagcgcc ccagcaaccc tgactccctg 890
ccagcacgtc caaggctgct taccccagca acctcccatc ccctgagccc tcaataaatg 950
ccatctgtag caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1010
aaaaaaaaaa aaaaaaa                                     1027
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Fig. 9 (2 of 2)